GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: February 13, 2001, 12:42:48 ; Search time 104.25 Seconds
(without alignments)
6824.989 Million cell updates/sec

Title: US-09-481-990-1
Perfect score: 1894
Sequence: 1 GGGCAGGAAGACGGCGCTGC.....ATAATAAAAAAAAAAAAAA 1894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1894	100.0	1894	18	T64960	TWIK-1 potassium c
2	383.2	20.2	758	21	A02285	Human colon cancer
3	237	12.5	2180	20	X78383	Human hTREK-1 cDNA
4	237	12.5	2571	20	Z11914	Human potassium ch
5	237	12.5	2671	21	Z46092	cDNA encoding KT4,
6	237	12.5	2735	21	Z46094	cDNA encoding KT5,
7	112.8	6.0	1551	21	Z98176	Human signal pepti
8	106.6	5.6	1182	21	A27105	Human h-TRAAK cDNA
9	106.6	5.6	1218	21	A27106	Human h-TRAAK cDNA
10	98.4	5.2	131	16	T22321	Human gene signatu
11	95	5.0	923	20	Z11904	Human potassium ch
12	95	5.0	1993	20	Z10607	cDNA encoding a me
13	95	5.0	1994	20	Z00040	Mouse h-TREK1 poly
14	80.6	4.3	1246	20	Z00039	h-TREK1 polynucleo
15	80.6	4.3	3300	20	Z11915	Human potassium ch
16	77.4	4.1	1497	21	A15943	Human protein clon
17	77.4	4.1	3768	21	A15953	Human protein clon
18	75.2	4.0	1794	20	Z10606	cDNA encoding a me
c 19	62.6	3.3	3198	20	X02974	Human IL-1ra BAC c
c 20	62.2	3.3	1337	20	Z17263	Human gene express
21	60.8	3.2	1368	20	X27398	Human secreted pro
c 22	60.4	3.2	2188	20	Z77506	Human ovarian tumo
23	59.6	3.1	2026	20	Z11734	Human transport-as
24	59.4	3.1	1028	13	Q27091	XTY26 probe. Homo
25	59	3.1	567	21	A29550	HIV codon altered
c 26	58.6	3.1	12001	16	Q76213	HSV L/ST region.
27	58.4	3.1	1000	21	A02484	Human colon cancer
28	58.2	3.1	4523	20	X00462	Human type V adeny
29	58	3.1	2923	11	Q06173	Human Bone Morphog
30	58	3.1	2923	13	Q32855	BMP6. Rattus ratt
31	58	3.1	2923	14	Q37568	Human BMP-6 coding
32	58	3.1	2923	14	Q41294	Human BMP-6 gene.
33	56.8	3.0	114955	20	X53491	Human adenosine A1
34	56.6	3.0	1127	21	A02477	Human colon cancer
c 35	56	3.0	114955	20	X53491	Human adenosine A1
36	54.6	2.9	1266	20	X09011	Brn-3a polynucleot
c 37	54.4	2.9	4423	17	T14914	cDNA encoding mult
38	54.4	2.9	4563	21	A37093	Human PRO1487 (UNQ
c 39	54.4	2.9	4669	17	T14913	cDNA encoding mult
c 40	54.4	2.9	4834	17	T14912	cDNA encoding mult
c 41	54.4	2.9	4864	17	T14911	cDNA encoding mult
c 42	54.4	2.9	4885	17	T14910	cDNA encoding mult
c 43	54.4	2.9	5011	15	Q65377	Multidrug resistan
c 44	54.4	2.9	5011	17	T17173	cDNA encoding mult
c 45	54.4	2.9	5011	19	V31497	Human multidrug re

ALIGNMENTS

RESULT 1
T64960
ID T64960 standard; cDNA; 1894 BP.
XX
AC T64960;
XX
DT 18-MAR-1998 (first entry)
XX
DE TWIK-1 potassium channel cDNA.
XX
KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
KW Tandem of P domains in a Weak Inward rectifying K+; antibody; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..1193
FT /*tag= a
FT /product= TWIK-1_potassium_channel_protein
XX
PN FR2744730-A1.
XX
PD 14-AUG-1997.
XX
PF 08-FEB-1996; 96FR-0001565.
XX
PR 08-FEB-1996; 96FR-0001565.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;
PI Lesage F, Romey g;
XX
DR WPI; 1997-427773/40.
DR P-PSDB; W23397.

XX
PT Nucleic acid encoding new potassium channel designated TWIK-1 -
PT useful for treating channel deficiency diseases, screening for
PT active agents and for diagnosis
XX
PS Claim 3; Figure 1b; 37pp; French.
XX
CC The present cDNA sequence encodes a protein comprising a potassium
CC channel with the properties of a TWIK (Tandem of P domains in
CC a Weak Inward rectifying K+)-1 channel. This is the first member of a new
CC family of channels consisting of 4 transmembrane segments and two P
CC domains, and being only weakly rectifying. The cDNA, vectors, the cells
CC expressing TWIK-1 type channels and the protein are used to compensate
CC for deficiency of potassium channels in various tissues. Compounds
CC for modulating activity of TWIK-1 type channels may also be useful
CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
CC disease, neurodegeneration (particularly of ischaemic or anoxic origin),
endocrine or muscular disorders. The cDNA and the vectors can also be
used to create transgenic animals (especially knock-out animals) for use
as models of TWIK-1 related diseases. Analysis of the sequence of the
CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
CC can be used to detect TWIK-1 channels and for inhibiting or activating
CC the channels in vivo.
XX
SQ Sequence 1894 BP; 461 A; 435 C; 512 G; 486 T; 0 other;

Query Match 100.0%; Score 1894; DB 18; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGCAGGAAGACGGCGCTGCCCGGAGGAGCGGGGCGGGCGGGCGCGCGGGGGAGCGGGCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gggcaggaagacggcgctgcccggaggagcggggcgggcgggcgcgcgggggagcgggcg 60

Qy     61 GCGGGCGGGAGCCAGGCCCGGGCGGGGGCGGGGGCGGCGGGGCCAGAAGAGGCGGCGGGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gcgggcgggagccaggcccgggcgggggcgggggcggcggggccagaagaggcggcgggc 120

Qy    121 CGCGCTCCGGCCGGTCTGCGGCGTTGGCCTTGGCTTTGGCTTTGGCGGCGGCGGTGGAGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 cgcgctccggccggtctgcggcgttggccttggctttggctttggcggcggcggtggaga 180

Qy    181 AGATGCTGCAGTCCCTGGCCGGCAGCTCGTGCGTGCGCCTGGTGGAGCGGCACCGCTCGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 agatgctgcagtccctggccggcagctcgtgcgtgcgcctggtggagcggcaccgctcgg 240

Qy    241 CCTGGTGCTTCGGCTTCCTGGTGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 cctggtgcttcggcttcctggtgctgggctacttgctctacctggtcttcggcgcagtgg 300

Qy    301 TCTTCTCCTCGGTGGAGCTGCCCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 tcttctcctcggtggagctgccctatgaggacctgctgcgccaggagctgcgcaagctga 360

Qy    361 AGCGACGCTTCTTGGAGGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 agcgacgcttcttggaggagcacgagtgcctgtctgagcagcagctggagcagttcctgg 420

Qy    421 GCCGGGTGCTGGAGGCCAGCAACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gccgggtgctggaggccagcaactacggcgtgtcggtgctcagcaacgcctcgggcaact 480

Qy    481 GGAACTGGGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ggaactgggacttcacctccgcgctcttcttcgccagcaccgtgctctccaccacaggtt 540

Qy    541 ATGGCCACACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 atggccacaccgtgcccttgtcagatggaggtaaggccttctgcatcatctactccgtca 600

Qy    601 TTGGCATTCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ttggcattcccttcaccctcctgttcctgacggctgtggtccagcgcatcaccgtgcacg 660

Qy    661 TCACCCGCAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 tcacccgcaggccggtcctctacttccacatccgctggggcttctccaagcaggtggtgg 720

Qy    721 CCATCGTCCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ccatcgtccatgccgtgctccttgggtttgtcactgtgtcctgcttcttcttcatcccgg 780

Qy    781 CCGCTGTCTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ccgctgtcttctcagtcctggaggatgactggaacttcctggaatccttttatttttgtt 840

Qy    841 TTATTTCCCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ttatttccctgagcaccattggcctggggattatgtgcctggggaaggctacaatcaaa 900

Qy    901 AATTCAGAGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 aattcagagagctctataagattgggatcacgtgttacctgctacttggccttattgcca 960

Qy    961 TGTTGGTAGTTCTGGAAACCTTCTGTGAACTCCATGAGCTGAAAAAATTCAGAAAAATGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 tgttggtagttctggaaaccttctgtgaactccatgagctgaaaaaattcagaaaaatgt 1020

Qy   1021 TCTATGTGAAGAAGGACAAGGACGAGGATCAGGTGCACATCATAGAGCATGACCAACTGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 tctatgtgaagaaggacaaggacgaggatcaggtgcacatcatagagcatgaccaactgt 1080

Qy   1081 CCTTCTCCTCGATCACAGACCAGGCAGCTGGCATGAAAGAGGACCAGAAGCAAAATGAGC 1140
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Db   1081 ccttctcctcgatcacagaccaggcagctggcatgaaagaggaccagaagcaaaatgagc 1140

Qy   1141 CTTTTGTGGCCACCCAGTCATCTGCCTGCGTGGATGGCCCTGCAAACCATTGAGCGTAGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 cttttgtggccacccagtcatctgcctgcgtggatggccctgcaaaccattgagcgtagg 1200

Qy   1201 ATTTGTTGCATTATGCTAGAGCACCAGGGTCAGGGTGCAAGGAAGAGGCTTAAGTATGTT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1261 CATTTTTATCAGAATGCAAAAGCGAAAATTATGTCACTTTAAGAAATAGCTACTGTTTGC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 cattttatcagaatgcaaaagcgaaaattatgtcactttaagaaatagctactgtttgc 1320

Qy   1321 AATGTCTTATTAAAAAACAACAAAAAAAAGACACATGGAACAAAGAAGCTGTGACCCCAGC 1380
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Db   1321 aatgtcttattaaaaaacaacaaaaaaaagacacatggaacaaagaagctgtgaccccagc 1380

Qy   1381 AGGATGTCTAATATGTGAGGAAATGAGATGTCCACCTAAAATTCATATGTGACAAAATTA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 aggatgtctaatatgtgaggaaatgagatgtccacctaaaattcatatgtgacaaaatta 1440

Qy   1441 TCTCGACCTTACATAGGAGGAGAATACTTGAAGCAGTATGCTGCTGTGGTTAGAAGCAGA 1500
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Db   1441 tctcgaccttacataggaggagaatacttgaagcagtatgctgctgtggttagaagcaga 1500

Qy   1501 TTTTATACTTTTAACTGGAAACTTTGGGGTTTGCATTTAGATCATTTAGCTGATGGCTAA 1560
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Db   1501 ttttatactttaactggaaactttggggtttgcatttagatcatttagctgatggctaa 1560

Qy   1561 ATAGCAAAATTTATATTTAGAAGCAAAAAAAAAAAGCATAGAGATGTGTTTTATAAATAG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 atagcaaaatttatatttagaagcaaaaaaaaaaagcatagagatgtgttttataaatag 1620

Qy   1621 GTTTATGTGTACTGGTTTGCATGTACCCACCCAAAATGATTATTTTTGGAGAATCTAAGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 gtttatgtgtactggtttgcatgtacccacccaaaatgattatttttggagaatctaagt 1680

Qy   1681 CAAACTCACTATTTATAATGCATAGGTAACCATTAACTATGTACATATAAAGTATAAATA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 caaactcactatttataatgcataggtaaccattaactatgtacatataaagtataaata 1740
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Qy   1741 TGTTTATATTCTGTACATATGGTTTAGGTCACCAGATCCTAGTGTAGTTCTGAAACTAAG 1800
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Qy   1801 ACTATAGATATTTTGTTTCTTTTGATTTCTCTTTATACTAAAGAATCCAGAGTTGCTACA 1860
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Db   1801 actatagatattttgtttcttttgatttctctttatactaaagaatccagagttgctaca 1860

Qy   1861 ATAAAATAAGGGGAATAATAAAAAAAAAAAAAAA 1894
          |||||||||||||||||||||||||||||||||
Db   1861 ataaaataaggggaataataaaaaaaaaaaaaaa 1894
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RESULT 2
A02285
ID A02285 standard; cDNA; 758 BP.
XX
AC A02285;
XX
DT 19-MAY-2000 (first entry)

Human colon cancer cell line polynucleotide sequence SEQ ID NO:2276.
XX
KW Human; colon cancer; tumour; diagnosis; gene expression product;
KW probe; detection; cancerous state; metastasis; identification;
KW breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9958675-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10602.
XX
PR 14-MAY-1998; 98US-0085426.
PR 15-MAY-1998; 98US-0085537.
PR 15-MAY-1998; 98US-0085696.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;

WPI; 2000-126369/11.
XX
PT Polynucleotide library used to determine cancerous states of mammalian
PT cells -
XX
PS Claim 1; Page 895; 1097pp; English.
XX
CC A00010 to A02716 represent polynucleotides isolated from cDNA libraries
CC constructed from human colon cancer cell lines. The present invention
CC also describes a method of detecting differentially expressed genes
CC correlated with a cancerous state of a mammalian cell, comprising
CC detecting at least one differentially expressed gene product in a test
CC sample derived from a cell suspected of being cancerous, where detection
CC of the differentially expressed gene product is correlated with a
CC cancerous state of the cell from which the test sample was derived.
CC The polynucleotides sequences can be used in a method for detecting
CC differentially expressed genes correlated with a cancerous state of a
CC mammalian cell. The polynucleotides can also be used as probes for
CC detecting and mapping related genes. They can be used in diagnosis and
CC prognosis of diseases and disorders (e.g. identification of
CC pre-metastatic or metastatic cancerous states, stages of cancer, or
CC responsiveness of cancer to therapy). This is particularly for breast
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC negative breast cancer, lung cancer, and colon cancer.
XX
SQ Sequence 758 BP; 200 A; 159 C; 131 G; 189 T; 79 other;

```
  Query Match             20.2%;  Score 383.2;  DB 21;  Length 758;
  Best Local Similarity   86.8%;  Pred. No. 2.3e-67;
  Matches  500;  Conservative    0;  Mismatches   66;  Indels   10;  Gaps    9;

Qy   1068 CATGACCAACTGTCCTTCTCCTCGATCACAGACCAGGCAGCTGGCATGAAAGAGGACCAG 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     23 catgaccaactgtccttctcctcgatcacagaccaggcagctggcatgaaagaggaccnn 82

Qy   1128 AAGCAAAATGAGCCTTTTGTGGCCACCCAGTCATCTGCCTGCGTGGATGGCCCTGCAAAC 1187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 aagcaaaatgagcctttgtggccacccagtcatctgcctgcgtggatggccctgcaaac 142

Qy   1188 CATTGAGCGTAGGATTTGTTGCATTATGCTAGAGCACCAGGGTCAGGGTGCAAGGAAGAG 1247
          |||||||||||||| |||||||||||||||||||||||| ||||||||| ||||||
Db    143 cattgagcgtaggatntgttgcattatgctagagcaccagggncagggtgcacggaagan 202

Qy   1248 GCTTAAGTATGTTCATTT-TTATCAGAATGCAAAAG-CGAAAATTATGTCACTTTAAGAA 1305
          ||| ||||||| | |||  |||||| |||||| ||| ||||||||||||| |||||||||
Db    203 gctcaagtatgnttattncttatcacaatgcanaagccgaaaattatgtcnctttaagaa 262

Qy   1306 ATAGCTA-CTGTTTGCAATGTCTTATTAAAAAACAACAAAAAAAGACACATGGAACAAAG 1364
          ||| ||| |||||||| ||||| |||||||||| ||||| ||||||| |||||||| ||
Db    263 atacctacctgtttgcnatgtcntattaaaaaacnacaaanaaagacaaatggaacanag 322

Qy   1365 -AAGCTGTGACCCCAGCAGGATGTCTAATATGTGAGGAAATGAGATGTCCACCTAAAATT 1423
           || |||||||||||||||||| | |||||||||||||||| ||| ||||||||| |
Db    323 aaanctgtgaccccagcaggatgncnaatatgtgaggaaatganatgcccacctaaaa-t 381

Qy   1424 CATATGTGACAAAATTATCTCGACCTTACATAGGAGGAGAATACTTGAAGCAGTATGCTG 1483
          |||||||| ||| |||||||||||||| |||| |||||||||||||| | | ||||||||
Db    382 catatgtg-caanattatctcgaccttccatangaggagaatacttgnancngtatgctg 440

Qy   1484 -CTGTGGTTAGAAGCAGATTTTATACTTTTAACTGGAAACTTTGGGGTTTGCATTTAGAT 1542
           |||| |||| ||||| |||||||||||||||||||||||| ||||||||    ||  ||
Db    441 cctgtngttanaagcaaattttatacttttaactggaaactntgggtttgcatttaat 500

Qy   1543 CATTTAGCTGATGGCTAAATAGCAA--AATTTATATTTAGAAGCAAAAAAAAAAAGCATA 1600
          |||||| |||| |||||||||||| |  | ||  | ||||||| |  |||||||   | ||
Db    501 catttaactgacggctaaatagccancatttntttttttagaanctnaaaaaaangcccta 560

Qy   1601 GAGATGT-GTTTTATAAATAGGTTTATGTGTACTGG 1635
          |   ||| | ||| ||||| || |||||   ||| |
Db    561 gnnctgtngntttntaaatnggnttatgcnnactcg 596
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RESULT 3
X78383
ID X78383 standard; cDNA to mRNA; 2180 BP.
XX
AC X78383;
XX
DT 25-AUG-1999 (first entry)
XX
DE Human hTREK-1 cDNA.
XX
KW hTREK-2; Twik-1 Related K+ channel-2; vasotropic; antiinflammatory;
KW analgesic; treatment; gene therapy; inhibitor; detection; diagnosis;
KW disease susceptibility; cerebral; cardiac; renal; ischemia; brain;
KW inflammation; pain; mimic; neurotransmitter; hormone; chromosome mapping;
KW linkage analysis; mutation; immunogen; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 74..1015
FT /*tag= a
FT /product= "hTREK-2"

XX
PN EP930364-A1.
XX
PD 21-JUL-1999.
XX
PF 16-JAN-1998; 98EP-0400072.
XX
PR 16-JAN-1998; 98EP-0400072.
XX
PA (SYNO) SYNTHELABO.
XX
PI Partiseti M;
XX
DR WPI; 1999-387707/33.
DR P-PSDB; Y25116.
XX
PT New human polypeptides useful for diagnosing and treating cerebral
PT and cardiac ischemias
XX
Claim 5; Page 15-18; 21pp; English.
XX
CC This invention describes a novel human Twik-1 Related K+ channel-2
CC (hTREK-2) polypeptide (I) and its encoding nucleic acid (II) which has
CC vasotropic, antiinflammatory and analgesic activity. (II) or agonists of
CC (I) may be used to stimulate production of (I) in vivo to treat patients
CC requiring enhanced activity or expression of (I). This use of (II)
CC represents a gene therapy regime. Antagonists of (I), the complement of
CC (II) used as an antisense construct or a polypeptide competitor of (I)
CC may be administered to patients to inhibit activity or expression of (I).
CC Detection of the presence or amount of (I) in a sample from a patient or
CC detection of mutations in (I) may be used to diagnose or measure
CC susceptibility to diseases related to altered expression or activity of
CC (I). The diseases and conditions resulting from altered activity or
CC expression of (I) which may be treated as above include cerebral,
CC cardiac and renal ischemias, brain and cardiac diseases, inflammation
CC and pain. In addition, (I), (II), and agonists and antagonists of (I)
CC may be used to mimic or antagonize the effects of endogenous
CC neurotransmitters and hormones. (II) or its fragments may be used as
CC hybridization probes to isolate full length and genomic cDNAs encoding
CC (I) or its homologues from cDNA or genomic libraries. (II) may also be
CC used for chromosome mapping and linkage analysis to identify the
CC relationship between genes and diseases which have been mapped to the
CC same chromosome. In addition (II) may be used to identify mutations
CC associated with diseases by comparing the sequence of (II) between
CC affected and unaffected individuals. (I) or its fragments may be used as
CC immunogens to produce antibodies against (I). Antibodies to (I) may be
CC used to isolate or identify clones expressing (I) or to purify (I) by
CC affinity chromatography. These antibodies may also be used to treat the
CC above diseases as agonists or antagonists of (I).
XX
SQ Sequence 2180 BP; 374 A; 669 C; 645 G; 492 T; 0 other;

Query Match 12.5%; Score 237; DB 20; Length 2180;
Best Local Similarity 56.9%; Pred. No. 3.2e-38;
Matches 463; Conservative 0; Mismatches 335; Indels 15; Gaps 1;

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Qy    203 CAGCTCGTGCGTGCGCCTGGTGGAGCGGCACCGCTCGGCCTGGTGCTTCGGCTTCCTGGT 262
          |||  |  |||  |  ||  |||||         ||   ||  |  |    | |    |    |
Db     46 cagggctcgcggggtcccggtgggtgccatgcggaggggcgcgcttctggcgggcgcctt 105

Qy    263 GCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGCC 322
          |   |  |||      ||||||||  | |||||  || |  |  |   | |||||  |||
Db    106 ggccgcgtacgccgcgtacctggtgctgggcgcgctgttggtggcgcggctggaggggcc 165

Qy    323 CTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGCA 382
            | || | |  ||| ||    ||||||   | ||||  |   |   |  |  ||
Db    166 gcacgaagccaggctccgagccgagctggagacgctgcgggcgcagctgcttcagcgcag 225

Qy    383 CGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCAA 442
          |  |||  || |||  |     |||||    ||| |||  || |||||||  |||| |
Db    226 cccgtgtgtggctgcccccgccctggacgccttcgtggagcgagtgctggcggccggacg 285
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Qy    443 CTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGAA----------CTG 487
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Qy    488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
          |||||||  |||| || ||||||||||||||||  || || |||||   || |||||  |
Db    346 ggacttcgcctctgctctcttcttcgccagcacgctgatcaccaccgtgggctatgggta 405

Qy    548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
          |||   |||  || | ||||  || ||||||||||| ||||  ||   |  || | ||| |
Db    406 cacaacgccactgactgatgcgggcaaggccttctccatcgcctttgcgctcctgggcgt 465

Qy    608 TCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCG 667
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Db    466 gccgaccaccatgctgctgctgaccgcctcagcccagcgcctgtcactgctgctgactca 525

Qy    668 CAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGT 727
          |  |||  |    |   |   ||| || |||||||    |   | |  || ||||  |
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Qy    728 CCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGT 787
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          |||  |   ||| |||||  | ||||| |||| |||| |||| || || || ||||| ||
Db    646 ctttgcccacctcgaggaggcctggagcttcttggatgccttctacttctgctttatctc 705

Qy    848 CCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAG 907
          |||  |||||| |||||||| || || ||||| ||||| | |       ||    | | |
Db    706 tctgtccaccatcggcctgggcgactacgtgcccggggaggcccctggccagccctaccg 765

Qy    908 AGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGT 967
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Qy    968 AGTTCTGGAAACCTTCTGTGAACTCCATGAGCT 1000
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Db    826 ggtgctgcagaccttccgccacgtgtccgacct 858
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RESULT 4
Z11914
ID Z11914 standard; cDNA; 2571 BP.
XX
AC Z11914;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K+Hnov49 cDNA.
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 110..1285
FT /*tag= a
FT /product= "Human K+Hnov49 potassium channel"
FT /note= "No stop codon given in specification"
FT variation 2186
FT /*tag= b
FT /rpt_unit= ATCT
FT /note= "Start site for repeats in 3' untranslated region"
XX
PN WO9943696-A1.
XX
PD 02-SEP-1999.
XX
PF 22-FEB-1999; 99WO-US03826.
XX
PR 19-JAN-1999; 99US-0116448.

```
PR   25-FEB-1998;   98US-0076687.
PR   07-AUG-1998;   98US-0095836.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; Y34132.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Claim 4; Page 99-101; 112pp; English.
XX
CC   This sequence represents human potassium channel K+Hnov49 cDNA.
CC   K+Hnov proteins have a high degree of homology to known potassium
CC   channels and may be alpha subunits, which form the functional channel, or
CC   accessory subunits that act to modulate the channel activity. K+Hnov49 is
CC   a 4 transmembrane domain, 2 pore domain potassium channel. The gene's
CC   chromosomal location is 1q41, determined via PCR chromosomal
CC   localisation using primers Z11937 and Z11938. K+Hnov cDNAs
CC   were isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS) disorders.
CC   Nucleotides encoding K+Hnov proteins may be used for identifying
CC   homologous or related proteins and the DNA sequences encoding them. They
CC   may be used to produce compositions that modulate the expression and
CC   function of the K+Hnov protein and in studying the biochemical pathways
CC   associated with it. They may also be used for the recombinant production
CC   of K+Hnov protein in fermentation cultures. Additionally, such
CC   nucleotides may be used in gene therapy protocols for the treatment
CC   of diseases associated with abnormal potassium channels.
XX
SQ   Sequence 2571 BP; 488 A; 744 C; 774 G; 565 T; 0 other;
```

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  Query Match             12.5%;  Score 237;  DB 20;  Length 2571;
  Best Local Similarity   56.9%;  Pred. No. 3.4e-38;
  Matches  463;  Conservative    0;  Mismatches  335;  Indels   15;  Gaps    1;

Qy     203 CAGCTCGTGCGTGCGCCTGGTGGAGCGGCACCGCTCGGCCTGGTGCTTCGGCTTCCTGGT 262
Db      82 cagggctcgcggggtcccggtgggtgccatgcggaggggcgcgcttctggcgggcgcctt 141

Qy     263 GCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGCC 322
Db     142 ggccgcgtacgccgcgtacctggtgctgggcgcgctgttggtggcgcggctggaggggcc 201

Qy     323 CTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGCA 382
Db     202 gcacgaagccaggctccgagccgagctggagacgctgcgggcgcagctgcttcagcgcag 261

Qy     383 CGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCAA 442
Db     262 cccgtgtgtggctgcccccgccctggacgccttcgtggagcgagtgctggcggccggacg 321

Qy     443 CTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGAA----------------CTG 487
Db     322 gctggggcgggtcgtgcttgctaacgcttcggggtccgccaagcgcctcggaccccgcctg 381

Qy     488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
Db     382 ggacttcgcctctgctctcttcttcgccagcacgctgatcaccaccgtgggctatgggta 441
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Qy     548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
Db     442 cacaacgccactgactgatgcgggcaaggccttctccatcgcctttgcgctcctgggcgt 501

Qy     608 TCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCG 667
Db     502 gccgaccaccatgctgctgctgaccgcctcagcccagcgcctgtcactgctgctgactca 561

Qy     668 CAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGT 727
Db     562 cgtgcccctgtcttggctgagcatgcgttggggctgggacccccggcgggcggcctgctg 621

Qy     728 CCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGT 787
Db     622 gcacttggtggccctgttgggggtcgtagtgaccgtctgctttctggtgccggctgtgat 681

Qy     788 CTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTC 847
Db     682 ctttgcccacctcgaggaggcctggagcttcttggatgccttctacttctgctttatctc 741

Qy     848 CCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAG 907
Db     742 tctgtccaccatcggcctgggcgactacgtgcccggggaggcccctggccagccctaccg 801

Qy     908 AGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGT 967
Db     802 ggccctctacaaggtgctggtcacagtctacctcttcctgggcctggtggccatggtgct 861

Qy     968 AGTTCTGGAAACCTTCTGTGAACTCCATGAGCT 1000
Db     862 ggtgctgcagaccttccgccacgtgtccgacct 894
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```
RESULT   5
Z46092
ID   Z46092 standard; cDNA; 2671 BP.
XX
AC   Z46092;
XX
DT   05-MAY-2000  (first entry)
XX
DE   cDNA encoding KT4, a TWIK family 2PD potassium channel polypeptide.
XX
KW   KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
KW   expressed sequence tag; EST; AA604914; ion channel dysfunction;
KW   renal disease; musculoskeletal disease; proliferative disease;
KW   renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW   muscular dystrophy; atherosclerosis; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             111..1052
FT                   /*tag= a
FT                   /product= "KT4"
XX
PN   WO200003687-A2.
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PD   27-JAN-2000.
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PF   20-JUL-1999;   99WO-US16471.
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PR   20-JUL-1998;   98US-0093486.
PR   13-AUG-1998;   98US-0096655.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Forsayeth JR,  Zhao BB,  Chavez RA;
XX
DR   WPI; 2000-171196/15.
DR   P-PSDB; Y68737.
XX
PT   Novel human potassium channel polynucleotides and polypeptides used in
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```
PT   the diagnosis, prevention and treatment of diseases including renal
PT   failure, cirrhosis, muscular dystrophy and cancers -
XX
PS   Claim 14; Fig 1A-C; 53pp; English.
XX
CC   The present sequence encodes a protein, designated KT4, which is a
CC   member of the TWIK family 2PD potassium channel polypeptides. These
CC   polypeptides contain two potential P-domains and 8 (preferably 4)
CC   transmembrane domains. The KT4 cDNA sequence was isolated from a brain
CC   cDNA library using degenerate oligonucleotides derived from human
CC   expressed sequence tag (EST) AA604914. The polypeptides and
CC   polynucleotides are used in the diagnosis, prevention and treatment of
CC   disease states. The polynucleotides may be used to detect and
CC   quantitate expression of TWIK family 2PD potassium channels, and
CC   aberrant or mutant forms of the polynucleotide which cause various
CC   diseases and disorders. Antisense oligonucleotides may be used to
CC   modulate the expression of polynucleotides of the invention. The
     polypeptides are used for treating diseases and disorders associated
     with ion channel dysfunction, including renal, musculoskeletal and
     proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC   dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
CC   and cancers.
XX
SQ   Sequence 2671 BP; 563 A; 743 C; 798 G; 567 T; 0 other;
```

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  Query Match             12.5%;  Score 237;  DB 21;  Length 2671;
  Best Local Similarity   56.9%;  Pred. No. 3.5e-38;
  Matches  463;  Conservative    0;  Mismatches  335;  Indels   15;  Gaps    1;

Qy     203 CAGCTCGTGCGTGCGCCTGGTGGAGCGGCACCGCTCGGCCTGGTGCTTCGGCTTCCTGGT 262
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Db      83 cagggctcgcggggtcccggtgggtgccatgcggaggggcgcgcttctggcgggcgcctt 142

Qy     263 GCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGCC 322
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Db     143 ggccgcgtacgccgcgtacctggtgctgggcgcgctgttggtggcgcggctggaggggcc 202

Qy     323 CTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGCA 382
             | || | |  ||| ||    ||||||   | ||||  |   |   |  |  ||
Db     203 gcacgaagccaggctccgagccgagctggagacgctgcgggcgcagctgcttcagcgcag 262

Qy     383 CGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCAA 442
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Db     263 cccgtgtgtggctgccccgccctggacgccttcgtggagcgagtgctggcggccggacg 322

Qy     443 CTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGAA----------------CTG 487
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Qy     488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
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Db     383 ggacttcgcctctgctctcttcttcgccagcacgctgatcaccaccgtgggctatgggta 442

Qy     548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
           |||   |||  || | ||||  || ||||||||||| ||||  ||   |  || | ||| |
Db     443 cacaacgccactgactgatgcgggcaaggccttctccatcgcctttgcgctcctgggcgt 502

Qy     608 TCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCG 667
            ||   |||| | ||| | |||||  ||    | |||||||  |  |  |||   | || |
Db     503 gccgaccaccatgctgctgctgaccgcctcagcccagcgcctgtcactgctgctgactca 562

Qy     668 CAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGT 727
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Db     563 cgtgcccctgtcttggctgagcatgcgttggggctgggacccccggcgggcggcctgctg 622

Qy     728 CCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGT 787
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Qy     848 CCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAG 907
           |||  |||||| |||||||| || || ||||| ||||| | |      ||    | | |
Db     743 tctgtccaccatcggcctgggcgactacgtgcccggggaggcccctggccagccctaccg 802

Qy     908 AGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGT 967
             |  ||||| ||| |   | ||||    |||||  | || |||||  | |||||| || |
Db     803 ggccctctacaaggtgctggtcacagtctacctcttcctgggcctggtggccatggtgct 862

Qy     968 AGTTCTGGAAACCTTCTGTGAACTCCATGAGCT 1000
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Db     863 ggtgctgcagaccttccgccacgtgtccgacct 895
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RESULT   6
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ID   Z46094 standard; cDNA; 2735 BP.
XX
AC   Z46094;
XX
DT   05-MAY-2000  (first entry)
XX
DE   cDNA encoding KT5, a TWIK family 2PD potassium channel polypeptide.
XX
KW   KT5; TWIK family 2PD potassium channel polypeptide; P-domain;
KW   expressed sequence tag; EST; AA533124; ion channel dysfunction;
KW   renal disease; musculoskeletal disease; proliferative disease;
KW   renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW   muscular dystrophy; atherosclerosis; cancer; ss.
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OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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PN   WO200003687-A2.
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XX
PR   20-JUL-1998;   98US-0093486.
PR   13-AUG-1998;   98US-0096655.
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PA   (ELAN-) ELAN PHARM INC.
XX
PI   Forsayeth JR,  Zhao BB,  Chavez RA;
XX
DR   WPI; 2000-171196/15.
DR   P-PSDB; Y68738.
XX
PT   Novel human potassium channel polynucleotides and polypeptides used in
PT   the diagnosis, prevention and treatment of diseases including renal
PT   failure, cirrhosis, muscular dystrophy and cancers -
XX
PS   Claim 15; Fig 3A-C; 53pp; English.
XX
CC   The present sequence encodes a protein, designated KT5, which is a
CC   member of the TWIK family 2PD potassium channel polypeptides. These
CC   polypeptides contain two potential P-domains and 8 (preferably 4)
CC   transmembrane domains. The KT4 cDNA sequence was isolated from a brain
CC   cDNA library using degenerate oligonucleotides derived from human
CC   expressed sequence tag (EST) AA533124. The polypeptides and
CC   polynucleotides are used in the diagnosis, prevention and treatment of
CC   disease states. The polynucleotides may be used to detect and
CC   quantitate expression of TWIK family 2PD potassium channels, and
CC   aberrant or mutant forms of the polynucleotide which cause various
CC   diseases and disorders. Antisense oligonucleotides may be used to
CC   modulate the expression of polynucleotides of the invention. The
CC   polypeptides are used for treating diseases and disorders associated
CC   with ion channel dysfunction, including renal, musculoskeletal and
```

```
CC   proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC   dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
CC   and cancers.
XX
SQ   Sequence 2735 BP; 572 A; 765 C; 822 G; 576 T; 0 other;


  Query Match             12.5%;  Score 237;  DB 21;  Length 2735;
  Best Local Similarity   56.9%;  Pred. No. 3.5e-38;
  Matches  463;  Conservative    0;  Mismatches  335;  Indels   15;  Gaps    1;

Qy    203 CAGCTCGTGCGTGCGCCTGGTGGAGCGGCACCGCTCGGCCTGGTGCTTCGGCTTCCTGGT 262
Db     95 cagggctcgcggggtcccggtgggtgccatgcggaggggcgcgcttctggcgggcgccctt 154

Qy    263 GCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGCC 322
Db    155 ggccgcgtacgccgcgtacctggtgctgggcgcgctgttggtggcgcggctggaggggcc 214

Qy    323 CTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGCA 382
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Qy    383 CGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCAA 442
Db    275 cccgtgtgtggctgcccccgccctggacgccttcgtggagcgagtgctggcggccggacg 334

Qy    443 CTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGAA----------------CTG 487
Db    335 gctggggcgggtcgtgcttgctaacgcttcggggtccgccaacgcctcggaccccgcctg 394

Qy    488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
Db    395 ggacttcgcctctgctctcttcttcgccagcacgctgatcaccaccgtgggctatgggta 454

Qy    548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
Db    455 cacaacgccactgactgatgcgggcaaggccttctccatcgcctttgcgctcctgggcgt 514

Qy    608 TCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCG 667
Db    515 gccgaccaccatgctgctgctgaccgcctcagcccagcgcctgtcactgctgctgactca 574

Qy    668 CAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGT 727
Db    575 cgtgcccctgtcttggctgagcatgcgttggggctgggaccccggcgggcggcctgctg 634

Qy    728 CCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGT 787
Db    635 gcacttggtggccctgttgggggtcgtagtgaccgtctgctttctggtgccggctgtgat 694

Qy    788 CTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTGTTTTATTTC 847
Db    695 ctttgcccacctcgaggaggcctggagcttcttggatgccttcttcacttctgctttatctc 754

Qy    848 CCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAG 907
Db    755 tctgtccaccatcggcctgggcgactacgtgcccggggaggcccctggccagccctaccg 814

Qy    908 AGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGT 967
Db    815 ggccctctacaaggtgctggtcacagtctacctcttcctgggcctggtggccatggtgct 874

Qy    968 AGTTCTGGAAACCTTCTGTGAACTCCATGAGCT 1000
Db    875 ggtgctgcagaccttccgccacgtgtccgacct 907


RESULT   7
Z98176
ID   Z98176 standard; cDNA; 1551 BP.
XX
AC   Z98176;
XX
DT   11-MAY-2000  (first entry)
XX
DE   Human signal peptide containing protein HSPP-68 cDNA SEQ ID NO:202.
XX
KW   Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW   inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW   antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW   antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW   reproductive disorder; developmental disorder; arteriosclerosis;
KW   cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW   asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW   Parkinson's disease; Huntington's diseases; ovulatory defect;
KW   muscular dystrophy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200000610-A2.
XX
PD   06-JAN-2000.
XX
PF   25-JUN-1999;   99WO-US14484.
XX
PR   26-JUN-1998;   98US-0090762.
PR   31-JUL-1998;   98US-0094983.
PR   01-OCT-1998;   98US-0102686.
PR   11-DEC-1998;   98US-0112129.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Tang YT,  Gorgone GA,  Corley NC,  Guegler KJ,  Baughn MR;
PI   Akerblom IE,  Au-Young J,  Yue H,  Patterson C,  Reddy R,  Hillman JL;
PI   Bandman O;
XX
DR   WPI; 2000-160673/14.
DR   P-PSDB; Y87291.
XX
PT   New human signal peptide-containing proteins useful in treatment,
PT   prevention and diagnosis of e.g. cancer, inflammation and
PT   cardiovascular disease -
XX
PS   Claim 9; Page 290; 327pp; English.
XX
CC   Z98109 to Z98242 encode Y87224 to Y87357 which represent the human
CC   signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC   anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC   neuroprotective, cardiovascular and antiasthmatic activities, and can
CC   be used in gene therapy. HSPPs can be used to treat or prevent disorders
CC   associated with decreased activity or function of HSPP. Antagonists of
CC   HSPP are used to treat or prevent disorders associated with increased
CC   activity or function of HSPP. Such diseases include cell proliferation
CC   (including cancer), inflammation, cardiovascular, neurological,
CC   reproductive or developmental disorders, (e.g. arteriosclerosis,
CC   cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC   asthma, Crohn's disease, microbial or other infections, congestive or
CC   ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC   diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC   nucleic acids can be used for the recombinant production of HSPP, for
CC   detecting HSPP in standard hybridisation and amplification assays (for
CC   diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC   or ribozyme therapeutics, for detecting related sequences or genetic
CC   variations, and for chromosomal mapping. HSPP are also used to raise
CC   specific antibodies (Ab) and to screen for agonists and antagonists
CC   (potential therapeutic agents). Ab are used to diagnose, or monitor,
CC   HSPP-related diseases (in usual immunoassays), as therapeutic
CC   antagonists, in competitive drug screens, and for purification of HSPP
CC   from natural sources.
XX
SQ   Sequence 1551 BP; 256 A; 550 C; 496 G; 249 T; 0 other;


  Query Match              6.0%;  Score 112.8;  DB 21;  Length 1551;
  Best Local Similarity   52.1%;  Pred. No. 1.3e-13;
```

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  Matches  302;  Conservative    0;  Mismatches  272;  Indels    6;  Gaps   2;

Qy     301 TCTTCTCCTCGGTGGAGCTGCCCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGA 360
           ||  || |  | ||| |    ||   |    |     ||   ||  |  || | ||||||
Db      78 tcacctacctgctggtgggcgccgcggtcttcgacgcgctggagtcggagcccgagctga 137

Qy     361 AGCGACGCTTCTTGGAGGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGG 420
             ||      |  |||||    |   | |     || |  ||   |  |  ||
Db     138 tcgagcggcagcggctggagctgcggcagcaggagctgcgggcgcgctacaacctcagcc 197

Qy     421 GCCGGGTGCTGGAGGCCAGCAACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACT 480
             | |     ||||      |   || ||||  |   ||||       |  || |  |
Db     198 agggcggctacgaggagctggagcgcgtcgtgctgcgcctcaagccgcacaaggccggcg 257

Qy     481 GGAACTGGGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTT 540
           | | |||  |||| ||  | |  ||| |||||||| ||||||  || ||||||  || |
Db     258 tgcagtggcgcttcgccggctccttctacttcgccatcaccgtcatcaccaccatcggct 317

       541 ATGGCCACACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCA 600
           | || ||| | |  |||    | ||||| || ||||  |||||||| |||||  |  |
Db     318 acgggcacgcggcacccagcacggatggcggcaaggtgttctgcatgttctacgcgctgc 377

Qy     601 TTGGCATTCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACG 660
           | ||||| ||  |||| ||| |  |  |   |    ||| | |||||||||  |      |
Db     378 tgggcatcccgctcacgctcgtcatgttccagagcctgggcgagcgcatcaacaccttgg 437

Qy     661 TCACCCGCAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGG 720
           | |  |    | | | |  | | |   |  |||| |           |  |||
Db     438 tga---ggtacctgctgcaccgcgccaagaaggggctgggcatgcggcgcgccgacgtgt 494

Qy     721 CCATCGTCCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGG 780
           |||| | | |    |||||| | || ||  || |     | ||    | | ||||   |
Db     495 ccatggccaacatggtgctcatcggcttcttctcgtgcatcagcacgctgtgcatcggcg 554

Qy     781 CCGCTGTCTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTT 840
           |||| | ||||||   ||   | ||  |||||| |||| |  |  |||  || |  || |
Db     555 ccgccgccttctc---ccactacgagcactggaccttcttccaggcctactactactgct 611

Qy     841 TTATTTCCCTGAGCACCATTGGCCTGGGGGATTATGTGCC 880
           | ||  |||| | |||||| ||| | || || || ||| |
Db     612 tcatcaccctcaccaccatcggcttcggcgactacgtggc 651


RESULT   8
A27105
ID   A27105 standard; cDNA; 1182 BP.
XX
AC   A27105;
XX
DT   04-AUG-2000  (first entry)
XX
DE   Human h-TRAAK cDNA sequence #1.
XX
KW   Human; h-TRAAK; potassium channel polypeptide;
KW   2P domain potassium channel; neurodegenerative disease; stroke;
KW   psychiatric disorder; neurological disorder; Gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1182
FT                   /*tag=  a
FT                   /product= h-TRAAK protein #1
XX
PN   WO200026253-A1.
XX
PD   11-MAY-2000.
XX
PF   03-NOV-1999;   99WO-GB03634.
XX
PR   03-NOV-1998;   98GB-0024048.
PR   07-OCT-1999;   99GB-0023668.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Duckworth DM;
XX
DR   WPI; 2000-365583/31.
DR   P-PSDB; Y94425.
XX
PT   Novel isolated h-TRAAK polypeptides belonging to the potassium channel
PT   family of polypeptides, useful for the diagnosis and treatment of
PT   h-TRAAK related disorders,e.g. depression and schizophrenia -
XX
PS   Claim 5; Page 21; 35pp; English.
XX
CC   Functional genomics was used to identify h-TRAAK polypeptides and
CC   h-TRAAK polynucleotides from human tissue samples. h-TRAAK
CC   polypeptides have homology to the 2P domain potassium channel family of
CC   polypeptides. The h-TRAAK polypeptides and polynucleotides may
CC   be used in diagnostic assays for conditions related to h-TRAAK
CC   imbalance and for identifying agonists and antagonists of h-TRAAK
CC   polypeptides. The h-TRAAK polypeptides and polynucleotides may also
CC   be useful for treatment and prevention (e.g. as vaccines) of certain
CC   diseases, such as pain, psychiatric disorders including depression and
CC   schizophrenia, neurodegenerative disease including Alzheimer's, stroke
CC   and head trauma and neurological disorders including migraine and
CC   epilepsy. The present sequence is human h-TRAAK-1 cDNA sequence #1.
XX
SQ   Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 other;


  Query Match             5.6%;  Score 106.6;  DB 21;  Length 1182;
  Best Local Similarity   49.9%;  Pred. No. 2e-12;
  Matches  330;  Conservative    0;  Mismatches  319;  Indels   12;  Gaps    2;

Qy     257 CCTGGTGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGA 316
           |||| ||  |     |||||| ||| |||| |  || ||  |||| |||    |  ||||
Db      24 cctgctggcgctggtcttgctttacttggtgtctggtgccctggtgttccgggccctgga 83

Qy     317 GCTGCCCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGA 376
           || |||| | ||| | | |   |    |||||||  |  || |          ||| ||
Db      84 gcagccccacgagcagcaggcccagagggagctgggggaggtccgagagaagttcctgag 143

Qy     377 GGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGC 436
           ||  ||   |||  ||   || ||| ||||||  |   || |      ||||   || ||
Db     144 ggcccatccgtgtgtgagcgaccaggagctgggcctcctcatcaaggaggtggctgatgc 203

Qy     437 CAGCAACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGA---------ACTG 487
           |        || | |         | |||| |  |  ||||| | |          |||
Db     204 cctgggaggggtgcggacccagaaaccaactcgaccagcaacagcagccactcagcctg 263

Qy     488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
           |||| |   |  |||  |||| ||| |  | ||| |  || ||||||  || ||||||
Db     264 ggacctgggcagcgccttctttttctcagggaccatcatcaccaccatcggctatggcaa 323

Qy     548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
               |  |      ||||||  ||      ||||||||||| | ||  |  |  | || ||
Db     324 tgtggccctgcgcacagatgccgggcgcctcttctgcatcttttatgcgctggtggggat 383

Qy     608 TCC---CTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCAC 664
           |||    ||     ||||  |      ||  | || || ||    | ||   |    |
Db     384 tccgctgtttgggatcctactggcaggggtcggggaccggctgggctcctccctgcgcca 443

Qy     665 CCGCAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCAT 724
             |||       | |  |   |  | ||     | |   |      | || | | |  |
Db     444 tggcatcggtcacattgaagccatcttcttgaagtggcacgtgccaccggagctagtaag 503

Qy     725 CGTCCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGC 784
             || |   | | | | |||    |  | |  |  | |    ||||  || || || || |
Db     504 agtgctgtcggcgatgcttttcctgctgatcggctgcctgctctttgtcctcacgcccac 563

Qy     785 TGTCTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTAT 844
             || | |     |     ||| ||||||| |   |||||  || | || |||    |  |
Db     564 gttcgtgttctgctatatggaggactggagcaagctggaggccatctactttgtcatagt 623
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Qy    845 TTCCCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATT 904
Db    624 gacgcttaccaccgtgggctttggcgactatgtggccggcgcggaccccaggcaggactc 683

Qy    905 C 905
Db    684 c 684


RESULT   9
A27106
ID   A27106 standard; cDNA; 1218 BP.
XX
AC   A27106;
XX
DT   04-AUG-2000  (first entry)
XX
DE   Human h-TRAAK cDNA sequence #2.
XX
KW   Human; h-TRAAK; potassium channel polypeptide;
KW   2P domain potassium channel; neurodegenerative disease; stroke;
KW   psychiatric disorder; neurological disorder; Gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             37..1218
FT                   /*tag= a
FT                   /product= h-TRAAK protein #2
XX
PN   WO200026253-A1.
XX
PD   11-MAY-2000.
XX
PF   03-NOV-1999;   99WO-GB03634.
XX
PR   03-NOV-1998;   98GB-0024048.
PR   07-OCT-1999;   99GB-0023668.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Duckworth DM;
XX
DR   WPI; 2000-365583/31.
DR   P-PSDB; Y94426.
XX
PT   Novel isolated h-TRAAK polypeptides belonging to the potassium channel
PT   family of polypeptides, useful for the diagnosis and treatment of
PT   h-TRAAK related disorders,e.g. depression and schizophrenia -
XX
CC   Claim 11; Pages 21 and 22; 35pp; English.
XX
CC   Functional genomics was used to identify h-TRAAK polypeptides and
CC   h-TRAAK polynucleotides from human tissue samples. h-TRAAK
CC   polypeptides have homology to the 2P domain potassium channel family of
CC   polypeptides. The h-TRAAK polypeptides and polynucleotides may
CC   be used in diagnostic assays for conditions related to h-TRAAK
CC   imbalance and for identifying agonists and antagonists of h-TRAAK
CC   polypeptides. The h-TRAAK polypeptides and polynucleotides may also
CC   be useful for treatment and prevention (e.g. as vaccines) of certain
CC   diseases, such as pain, psychiatric disorders including depression and
CC   schizophrenia, neurodegenerative disease including Alzheimer's, stroke
CC   and head trauma and neurological disorders including migraine and
CC   epilepsy. The present sequence is human h-TRAAK cDNA sequence #2.
XX
SQ   Sequence 1218 BP; 182 A; 421 C; 395 G; 220 T; 0 other;


  Query Match             5.6%;  Score 106.6;  DB 21;  Length 1218;
  Best Local Similarity   49.9%;  Pred. No. 2e-12;
  Matches  330;  Conservative    0;  Mismatches  319;  Indels   12;  Gaps    2;

Qy    257 CCTGGTGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGA 316
Db     60 cctgctggcgctggtcttgctttacttggtgtctggtgccctggtgttccgggccctgga 119

Qy    317 GCTGCCCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGA 376
Db    120 gcagccccacgagcagcaggcccagagggagctgggggaggtccgagagaagttcctgag 179

Qy    377 GGAGCACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGC 436
Db    180 ggcccatccgtgtgtgagcgaccaggagctgggcctcctcatcaaggaggtggctgatgc 239

Qy    437 CAGCAACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGA---------ACTG 487
Db    240 cctgggaggggtgcggacccagaaaccaactcgaccagcaacagcagccactcagcctg 299

Qy    488 GGACTTCACCTCCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCA 547
Db    300 ggacctgggcagcgccttctttttctcagggaccatcatcaccaccatcggctatggcaa 359

Qy    548 CACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCAT 607
Db    360 tgtggccctgcgcacagatgccgggcgcctcttctgcatcttttatgcgctggtggggat 419

Qy    608 TCC---CTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGCACGTCAC 664
Db    420 tccgctgtttgggatcctactggcaggggtcggggaccggctgggctcctccctgcgcca 479

Qy    665 CCGCAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCAT 724
Db    480 tggcatcggtcacattgaagccatcttcttgaagtggcacgtgccaccggagctagtaag 539

Qy    725 CGTCCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGC 784
Db    540 agtgctgtcggcgatgcttttcctgctgatcggctgcctgctctttgtcctcacgcccac 599

Qy    785 TGTCTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTAT 844
Db    600 gttcgtgttctgctatatggaggactggagcaagctggaggccatctactttgtcatagt 659

Qy    845 TTCCCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATT 904
Db    660 gacgcttaccaccgtgggctttggcgactatgtggccggcgcggaccccaggcaggactc 719

Qy    905 C 905
Db    720 c 720


RESULT  10
T22321
ID   T22321 standard; cDNA to mRNA; 131 BP.
XX
AC   T22321;
XX
DT   13-SEP-1996  (first entry)
XX
DE   Human gene signature HUMGS03894.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
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PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 1099; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in T19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
     sequences were obtained from 3'-directed cDNA libraries prepared
     from various human tissues; synthesis of cDNA was initiated from the
     3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 131 BP; 50 A; 17 C; 19 G; 43 T; 2 other;
```

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  Query Match             5.2%;  Score 98.4;  DB 16;  Length 131;
  Best Local Similarity   97.1%;  Pred. No. 4.1e-11;
  Matches   99;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1781 AGTGTAGTTCTGAAACTAAGACTATAGATATTTTGTTTCTTTTGATTTCTCTTTATACTA 1840
           ||||||||||||||||||||||||||||||||  |||||||| ||||||||||||||||
Db       8 agtgtagttctgaaactaagactatagatatttnntttcttttaatttctctttatacta 67

Qy    1841 AAGAATCCAGAGTTGCTACAATAAAATAAGGGGAATAATAAA 1882
           |||||||||||||||||||||||||||||||||||||||||||
Db      68 aagaatccagagttgctacaataaaataaggggaataataaa 109
```

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RESULT  11
Z11904
     Z11904 standard; cDNA; 923 BP.
XX
AC   Z11904;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov2 cDNA.
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             165..758
FT                   /*tag=  a
FT                   /product= "Human K+Hnov2 potassium channel"
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US03826.
XX
PR   19-JAN-1999;   99US-0116448.
PR   25-FEB-1998;   98US-0076687.
PR   07-AUG-1998;   98US-0095836.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; Y34126.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Claim 4; Page 66-67; 112pp; English.
XX
CC   This sequence represents human potassium channel K+Hnov2 cDNA.
CC   K+Hnov proteins have a high degree of homology to known potassium
CC   channels and may be alpha subunits, which form the functional channel, or
CC   accessory subunits that act to modulate the channel activity. K+Hnov2 is
CC   a 4 transmembrane domain, 2 pore domain potassium channel. K+Hnov cDNAs
CC   were isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS) disorders.
CC   Nucleotides encoding K+Hnov proteins may be used for identifying
CC   homologous or related proteins and the DNA sequences encoding them. They
CC   may be used to produce compositions that modulate the expression and
CC   function of the K+Hnov protein and in studying the biochemical pathways
CC   associated with it. They may also be used for the recombinant production
CC   of K+Hnov protein in fermentation cultures. Additionally, such
CC   nucleotides may be used in gene therapy protocols for the treatment
CC   of diseases associated with abnormal potassium channels.
XX
SQ   Sequence 923 BP; 179 A; 267 C; 299 G; 178 T; 0 other;
```

```
  Query Match             5.0%;  Score 95;  DB 20;  Length 923;
  Best Local Similarity   53.3%;  Pred. No. 3.6e-10;
  Matches  250;  Conservative    0;  Mismatches  210;  Indels    9;  Gaps    2;

Qy     538 GTTATGGCCACACCGTGCCCTTGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCG 597
           ||||||||||||  |  ||  | ||    || || ||||||||||||||  ||||  | |
Db     154 gttatggccacatggccccactatcgccaggcggaaaggccttctgcatggtctatgcag 213

Qy     598 TCATTGGCATTCCCTTCACCCTCCTGTTCCTGACGGCTGTGGTCCAGCGCATCACCGTGC 657
           | | ||  | ||   | || |     || || |  |  ||  |||  || |    |||
Db     214 ccctggggctgccagcctccttagctctcgtggccaccctgcgccattgcctgc---tgc 270

Qy     658 ACGTCACCCGCAGGCCGGTCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGG 717
             ||   | || | ||      ||   |     ||| ||||   | ||  |     ||
Db     271 ctgtgctcagccgcccacgtgcctgggtagcggtccactggcagctgtcaccggccaggg 330

Qy     718 TGGCCATCGTCCATGCCGTGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCC 777
           ||  |  | || || ||    || ||  |  |    |    | ||||  |  |  | |
Db     331 ctgcgctgctgcaggcagttgcactgggactgctggtggccagcagctttgtgctgctgc 390

Qy     778 CGGCCGCTGTCTTCTCAGTCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTT 837
           | ||    ||  | |  | |||  |||  ||||| | | | ||||   || | || || |
Db     391 cagcgctggtgctgtggggccttcagggcgactgcagcctgctgggggccgtctacttct 450

Qy     838 GTTTTATTTCCCTGAGCACCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACA--- 894
           | || |  || || |||||||||||||||| ||| |   |||| ||    |||  ||
Db     451 gcttcagctcgctcagcaccattggcctggaggacttgctgcccggccgcggccgcagcc 510

Qy     895 ---ATCAAAAATTCAGAGAGCTCTATAAGATTGGGATCACGTGTTACCTGCTACTTGGCC 951
             | |      |     | ||     || | |   |     ||||| |||| || || |
Db     511 tgcaccccgtgatttaccacctgggccagctcgcacttcttggttacttgcttctaggac 570
```

```
Qy    952 TTATTGCCATGTTGGTAGTTCTGGAAACCTTCTGTGAACTCCATGAGCT 1000
          |  | ||||||  || | |   |||| |||||||  ||| || |   || |
Db    571 tcttggccatgctgctggcagtggagaccttctctgagctgccgcaggt 619


RESULT  12
Z10607
ID   Z10607 standard; cDNA; 1993 BP.
XX
AC   Z10607;
XX
DT   18-NOV-1999  (first entry)
XX
DE   cDNA encoding a mechanically sensitive potassium channel protein TREK-1.
XX
KW   Mechanically sensitive potassium channel protein; TREK-1;
KW   polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
KW   nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW   neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
KW   muscular disease; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             484..1596
FT                   /*tag=  a
XX
PN   WO9945108-A2.
XX
PD   10-SEP-1999.
XX
PF   23-FEB-1999;   99WO-FR00404.
XX
PR   05-MAR-1998;   98FR-0002725.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Honore E,  Fink M,  Lazdunski M,  Lesage F,  Duprat F;
XX
DR   WPI; 1999-551038/46.
DR   P-PSDB; Y30648.
XX
PT   New mechanically sensitive potassium channel, used to screen for
PT   specific modulators, potential therapeutic agents for heart and nervous
PT   system disorders  -
XX
PS   Claim 7; Page 23-25; 40pp; French.
XX
CC   The present sequence encodes a mechanically sensitive potassium
CC   channel protein designated TREK-1. The protein is activated by
CC   polyunsaturated fatty acids, particularly arachidonic acid, and by
CC   riluzole. The protein is used to screen for specific modulators which
CC   are useful for treating or preventing diseases of the heart and nervous
CC   systems in humans and animals, e.g. epilepsy, cardiovascular disease
CC   (arrhythmia), neurodegeneration (particularly where associated with
CC   ischemia or anoxia), abnormalities of hormone secretion and muscular
CC   disease. The protein itself may be used to treat these diseases.
CC   Antibodies specific for the protein are used to detect it in tissues,
CC   also as therapeutic inhibitors or activators.
XX
SQ   Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 other;


  Query Match             5.0%;  Score 95;  DB 20;  Length 1993;
  Best Local Similarity   48.7%;  Pred. No. 4.7e-10;
  Matches  350;  Conservative    0;  Mismatches  360;  Indels    9;  Gaps    3;

Qy    262 TGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGC 321
          | ||||    | | |||||||||| || |||| || | ||| |||    |  |||||| ||
Db    635 tcctggtggtcgtcctctacctgatcatcggagccgcggtgttcaaggcattggagcagc 694

Qy    322 CCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGC 381
          |  | |||      | | |        |    |  | |||||    |||| | |   |||
Db    695 ctcaggagatttcccagaggaccaccattgtgatccagaagcagaccttcatagcccagc 754

Qy    382 ACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCA 441
          | |  ||| |           |||||||  |  || |    |  |  |||  || | |
Db    755 atgcctgcgtcaactccaccgagctggacgaactcatccagcaaatagtggcagcaataa 814

Qy    442 ACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGA---ACTGGGACTTCACCT 498
          ||   ||  |         |  | |||  |||     |.   |   |||||||| ||
Db    815 acgcagggattatccccttaggaaacagctccaatcaagttagtcactgggacctcggaa 874

Qy    499 CCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCACACCGTGCCCT 558
           | |  ||||||| ||  | || ||  || | |||| ||| | |||  ||| |   ||
Db    875 gctctttcttctttgctggtactgttatcacaaccataggatttggaaacatctccccac 934

Qy    559 TGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCATTCCCTTCACCC 618
          | || || || ||    |||||||||||||  || |  | || ||||| ||
Db    935 gaactgaaggtggaaaaatattctgcatcatctatgccttgctgtgggaattcccctctttg 994

Qy    619 TCCTGTTCCTGAC---GGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCGCAGGCCGG 675
          | |  | ||| |   || ||  |  ||||     ||  |    |  |   | |   |
Db    995 gctttctactggctggggttggtgatcagctaggaactatatttggaaaaggaattgcca 1054

Qy    676 TCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGTCCATGCCG 735
          |  |   |    |      | |       |  |||  |  |       ||    ||
Db   1055 aagtggaagacacatttattaagtggaatgttagtcagacgaagattcgtatcatctcca 1114

Qy    736 TGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGTCTTCTCAG 795
          || |     |  |   ||  |    | ||||  |    |   |  || ||| | |
Db   1115 ccatcatcttcatcctgtttggctgtgtcctctttgtggctctccctgcggtcatattca 1174

Qy    796 TCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTCCCTGAGCA 855
          |     || | ||||| |  ||||||  |  | ||||||    ||||  | ||||  |
Db   1175 agcacatagaaggctggagcgccctggacgctatctatttgtggttatcactctgacga 1234

Qy    856 CCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAGAGAGCTCT 915
          |||||||  | || || || ||| | || | |    ||| | || |  |    ||  |||
Db   1235 ccattggatttggagactacgtggcaggtggatcagacattgaatatct---ggacttct 1291

Qy    916 ATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGTAGTTCTG 974
          | |||  || | |   ||  |   | ||  |||| ||      | |   |  ||||||
Db   1292 acaagcctgtggtgtggttctggatcctcgttgggctggcctactttgcagctgttctg 1350


RESULT  13
Z00040
ID   Z00040 standard; DNA; 1994 BP.
XX
AC   Z00040;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Mouse h-TREK1 polynucleotide.
XX
KW   h-TREK1; two pore potassium channel; inflammatory disease;
KW   chromosome 1q32; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             484..1719
FT                   /*tag=  a
FT                   /product= "h-TREK1"
XX
PN   WO9937762-A1.
XX
PD   29-JUL-1999.
XX
PF   02-DEC-1998;   98WO-EP07805.
XX
PR   09-OCT-1998;   98GB-0022135.
PR   27-JAN-1998;   98EP-0300570.
XX
```

PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Meadows HJ;
XX
DR WPI; 1999-469126/39.
DR P-PSDB; Y28497.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
PT pulmonary, cardiovascular and inflammatory diseases
XX
PS Claim 9; Page 25-26; 44pp; English.
XX
CC This sequence is the h-TREK1 polynucleotide from the mouse, encoding the
CC h-TREK1 polypeptide Y28496. h-TREK1 is a two pore potassium channel.
CC The polynucleotide sequence of h-TREK1 can be used to diagnose a disease
CC or susceptibility to a disease related to expression or activity of
CC h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC treatment of diseases including cancer, pulmonary, cardiovascular, and
CC inflammatory diseases, pain, psychiatric disorders including depression
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC stroke, and head trauma and neurological disorders including migraine.
XX
SQ Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 other;

Query Match 5.0%; Score 95; DB 20; Length 1994;
Best Local Similarity 48.7%; Pred. No. 4.7e-10;
Matches 350; Conservative 0; Mismatches 360; Indels 9; Gaps 3;

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Qy     262 TGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGC 321
           | ||||    | | |||||||||| || |||| || | ||| |||    |  |||||| ||
Db     635 tcctggtggtcgtcctctacctgatcatcggagccgcggtgttcaaggcattggagcagc 694

Qy     322 CCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGC 381
           |  | |||      | | |        |    | | |||||    |||| | |   |||
Db     695 ctcaggagatttcccagaggaccaccattgtgatccagaagcagaccttcatagcccagc 754

Qy     382 ACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCA 441
           | |  ||| |          |||||||  |  || |    |   |  |||  || | |
Db     755 atgcctgcgtcaactccaccgagctggacgaactcatccagcaaatagtggcagcaataa 814

Qy     442 ACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAACTGGA---ACTGGGACTTCACCT 498
           ||   ||  |        |  | |||  |||      |    |   ||||||||  ||
Db     815 acgcagggattatccccttaggaaacagctccaatcaagttagtcactgggacctcggaa 874

Qy     499 CCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCACACCGTGCCCT 558
           | |  ||||||| ||  | || ||  || | |||| ||| | |||  ||| |   ||
Db     875 gctctttcttctttgctggtactgttatcacaaccataggatttggaaacatctccccac 934

Qy     559 TGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCATTCCCTTCACCC 618
           | || || || ||    ||||||||||||||  || |  | || |||||| ||
Db     935 gaactgaaggtggaaaaatattctgcatcatctatgccttgctgggaattcccctctttg 994

Qy     619 TCCTGTTCCTGAC---GGCTGTGGTCCAGCGCATCACCGTGCACGTCACCCGCAGGCCGG 675
           | |  | |||  |   || ||  |  ||||     ||  |    |  |   | |   |
Db     995 gctttctactggctggggttggtgatcagctaggaactatatttggaaaaggaattgcca 1054

Qy     676 TCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGTCCATGCCG 735
           |  |   |    |      | |       |  |||  | |       ||    ||
Db    1055 aagtggaagacacatttattaagtggaatgttagtcagacgaagattcgtatcatctcca 1114

Qy     736 TGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGTCTTCTCAG 795
           || |     |  |   ||  |    | ||||  |     |   | || ||| | |
Db    1115 ccatcatcttcatcctgtttggctgtgtcctctttgtggctctccctgcggtcatattca 1174

Qy     796 TCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTCCCTGAGCA 855
           |     || | ||||| |  |||||  |  | ||||||    ||||  | ||||  |
Db    1175 agcacatagaaggctggagcgccctggacgctatctattttgtggttatcactctgacga 1234

Qy     856 CCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAGAGAGCTCT 915
           |||||||  | || || || ||| | || | |    ||| | || |  |    ||  |||
Db    1235 ccattggatttggagactacgtggcaggtggatcagacattgaatatct---ggacttct 1291
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Qy     916 ATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGTAGTTCTG 974
           | |||  || | |   ||  |   | ||  |||| ||      | |    |  ||||||
Db    1292 acaagcctgtggtgtggttctggatcctcgttgggctggcctactttgcagctgttctg 1350
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RESULT 14
Z00039
ID Z00039 standard; DNA; 1246 BP.
XX
AC Z00039;
XX
DT 12-OCT-1999 (first entry)
XX
DE h-TREK1 polynucleotide.
XX
KW h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome 1q32; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..1244
FT /*tag= a
FT /product= "h-TREK1"
XX
PN WO9937762-A1.
XX
PD 29-JUL-1999.
XX
PF 02-DEC-1998; 98WO-EP07805.
XX
PR 09-OCT-1998; 98GB-0022135.
PR 27-JAN-1998; 98EP-0300570.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Meadows HJ;
XX
DR WPI; 1999-469126/39.
DR P-PSDB; Y28496.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
PT pulmonary, cardiovascular and inflammatory diseases
XX
PS Claim 9; Page 24; 44pp; English.
XX
CC This sequence is the h-TREK1 polynucleotide, encoding the h-TREK1
CC polypeptide Y28496. h-TREK1 is a two pore potassium channel, and the gene
CC maps to human chromosome 1q32, between the markers D1S237 and WI5105. The
CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or
CC susceptibility to a disease related to expression or activity of h-TREK-1
CC polypeptides. The methods of diagnosis may be used in the treatment of
CC diseases including cancer, pulmonary, cardiovascular, and inflammatory
CC diseases, pain, psychiatric disorders including depression and
CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,
CC and head trauma and neurological disorders including migraine.
XX
SQ Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 other;

Query Match 4.3%; Score 80.6; DB 20; Length 1246;
Best Local Similarity 47.4%; Pred. No. 2.9e-07;
Matches 341; Conservative 0; Mismatches 369; Indels 9; Gaps 3;

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Qy     262 TGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGC 321
           | ||||      | ||||| ||| || |||| ||    || |||    |  |||||| ||
Db     160 tcctggtggttgtcctctatctgatcatcggagccaccgtgttcaaagcattggagcagc 219

Qy     322 CCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGC 381
           |  |||||      | | |        |    |  |||||| |   ||| |     | |
Db     220 ctcatgagatttcacagaggaccaccattgtgatccagaagcaaacattcatatcccaac 279

Qy     382 ACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCA 441
```

```
Db    280 attcctgtgtcaattcgacggagctggatgaactcattcagcaaatagtggcagcaataa 339

Qy    442 ACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAA---CTGGAACTGGGACTTCACCT 498
Db    340 atgcagggattataccgttaggaaacacctccaatcaaatcagtcactgggatttgggaa 399

Qy    499 CCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCACACCGTGCCCT 558
Db    400 gttccttcttctttgctggcactgttattacaaccataggatttggaaacatctcaccac 459

Qy    559 TGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCATTCCCTTCACCC 618
Db    460 gcacagaaggcggcaaaatattctgtatcatctatgccttactgggaattcccctctttg 519

Qy    619 TCCTGTTCCTGACGGCTGTGGT---CCAGCGCATCACCGTGCACGTCACCCGCAGGCCGG 675
Db    520 gttttctcttggctggagttggagatcagctaggcaccatatttggaaaaggaattgcca 579

Qy    676 TCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGTCCATGCCG 735
Db    580 aagtggaagatacgtttattaagtggaatgttagtcagaccaagattcgcatcatctcaa 639

Qy    736 TGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGTCTTCTCAG 795
Db    640 caatcatatttatactatttggctgtgtactctttgtggctctgcctgcgatcatattca 699

Qy    796 TCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTCCCTGAGCA 855
Db    700 aacacatagaaggctggagtgccctggacgccatttattttgtggttatcactctaacaa 759

Qy    856 CCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAGAGAGCTCT 915
Db    760 ctattggatttggtgactacgttgcaggtggatccgatattgaatatct---ggacttct 816

Qy    916 ATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGTAGTTCTG 974
Db    817 ataagcctgtcgtgtggttctggatccttgtagggcttgcttactttgctgctgtcctg 875
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```
RESULT  15
Z11915
ID   Z11915 standard; cDNA; 3300 BP.
XX
AC   Z11915;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov59 cDNA.
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             50..1285
FT                   /*tag= a
FT                   /product= "Human K+Hnov59 potassium channel"
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US03826.
XX
PR   19-JAN-1999;   99US-0116448.
PR   25-FEB-1998;   98US-0076687.
PR   07-AUG-1998;   98US-0095836.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; Y34133.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Claim 4; Page 102-104; 112pp; English.
XX
CC   This sequence represents human potassium channel K+Hnov59 cDNA.
CC   K+Hnov proteins have a high degree of homology to known potassium
CC   channels and may be alpha subunits, which form the functional channel, or
CC   accessory subunits that act to modulate the channel activity. K+Hnov59 is
CC   a 4 transmembrane domain, 2 pore domain potassium channel. The gene is
CC   located on chromosome 19, determined via PCR chromosomal
CC   localisation using primers Z11939 and Z11940. K+Hnov cDNAs
CC   were isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS) disorders.
CC   Nucleotides encoding K+Hnov proteins may be used for identifying
CC   homologous or related proteins and the DNA sequences encoding them. They
CC   may be used to produce compositions that modulate the expression and
CC   function of the K+Hnov protein and in studying the biochemical pathways
CC   associated with it. They may also be used for the recombinant production
CC   of K+Hnov protein in fermentation cultures. Additionally, such
CC   nucleotides may be used in gene therapy protocols for the treatment
CC   of diseases associated with abnormal potassium channels.
XX
SQ   Sequence 3300 BP; 997 A; 629 C; 680 G; 994 T; 0 other;
```

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  Query Match             4.3%;  Score 80.6;  DB 20;  Length 3300;
  Best Local Similarity   47.4%;  Pred. No. 3.9e-07;
  Matches  341;  Conservative    0;  Mismatches  369;  Indels    9;  Gaps    3;

Qy    262 TGCTGGGCTACTTGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGC 321
Db    201 tcctggtggttgtcctctatctgatcatcggagccaccgtgttcaaagcattggagcagc 260

Qy    322 CCTATGAGGACCTGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGC 381
Db    261 ctcatgagatttcacagaggaccaccattgtgatccagaagcaaacattcatatcccaac 320

Qy    382 ACGAGTGCCTGTCTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCA 441
Db    321 attcctgtgtcaattcgacggagctggatgaactcattcagcaaatagtggcagcaataa 380

Qy    442 ACTACGGCGTGTCGGTGCTCAGCAACGCCTCGGGCAA---CTGGAACTGGGACTTCACCT 498
Db    381 atgcagggattataccgttaggaaacacctccaatcaaatcagtcactgggatttgggaa 440

Qy    499 CCGCGCTCTTCTTCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCACACCGTGCCCT 558
Db    441 gttccttcttctttgctggcactgttattacaaccataggatttggaaacatctcaccac 500

Qy    559 TGTCAGATGGAGGTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCATTCCCTTCACCC 618
Db    501 gcacagaaggcggcaaaatattctgtatcatctatgccttactgggaattcccctctttg 560

Qy    619 TCCTGTTCCTGACGGCTGTGGT---CCAGCGCATCACCGTGCACGTCACCCGCAGGCCGG 675
Db    561 gttttctcttggctggagttggagatcagctaggcaccatatttggaaaaggaattgcca 620

Qy    676 TCCTCTACTTCCACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGTCCATGCCG 735
```

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Db    621 aagtggaagatacgtttattaagtggaatgttagtcagaccaagattcgcatcatctcaa 680

Qy    736 TGCTCCTTGGGTTTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGTCTTCTCAG 795

Db    681 caatcatatttatactatttggctgtgtactctttgtggctctgcctgcgatcatattca 740

Qy    796 TCCTGGAGGATGACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTCCCTGAGCA 855

Db    741 aacacatagaaggctggagtgccctggacgccatttattttgtggttatcactctaacaa 800

Qy    856 CCATTGGCCTGGGGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAGAGAGCTCT 915

Db    801 ctattggatttggtgactacgttgcaggtggatccgatattgaatatct---ggacttct 857

Qy    916 ATAAGATTGGGATCACGTGTTACCTGCTACTTGGCCTTATTGCCATGTTGGTAGTTCTG 974

Db    858 ataagcctgtcgtgtggttctggatccttgtagggcttgcttactttgctgctgtcctg 916
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Search completed: February 13, 2001, 19:46:07
Job time: 25399 sec